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10/032,717	10/23/2001	Andre R. Abad	35718/237005 (5718-118)	5409

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EXAMINER

KUBELIK, ANNE R

ART UNIT PAPER NUMBER

1638

DATE MAILED: 05/06/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

# Office Action Summary

Application No.

10/032,717

Applicant(s)

ABAD ET AL.

Examiner

Anne R. Kubelik

Art Unit

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --  
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

## Status

- 1) ☒ Responsive to communication(s) filed on 21 January 2005.
- 2a) ☒ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

## Disposition of Claims

- 4) ☒ Claim(s) 1-3,9-12,17-19,38-40,43-46,49-52 and 55-65 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-3,9-12,17-19,38,43,46,49,52 and 55-65 is/are rejected.
- 7) ☒ Claim(s) 39,40,44,45,50 and 51 is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

## Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

## Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

## Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)  
Paper No(s)/Mail Date \_\_\_\_\_
- 4) ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: search notes.

**DETAILED ACTION**

1. Claims 1-3, 9-12, 17-19, 38-40, 43-46, 49-52 and 55-65 are pending.
2. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.
3. The rejection of claims 1-3, 9-12, 17-19, 46, 52, 57 and 60-62 under 35 U.S.C. 103(a) as being unpatentable over Michaels et al (1996, US Patent 5,554,534) is withdrawn in light of the analysis and Declarations of Drs. McNeill and C Simmons.

***Claim Rejections - 35 USC § 112***

4. Claims 1-3, 9-12, 17-19, 38, 43, 46, 49, 52 and 55-65 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for nucleic acids encoding SEQ ID NO:2 and 10, expression cassettes comprising the nucleic acids, plants and seeds comprising a construct comprising the nucleic acid, and a method of using it to impact a plant pest, does not reasonably provide enablement for any nucleic acid that has 90% identity to SEQ ID NO:1, expression cassettes comprising the nucleic acid, plants and seeds comprising a construct comprising the nucleic acid and a method of using it to impact a plant pest. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims. The rejection is modified from the rejection set forth in the Office action mailed 21 October 2004, as applied to claims 1-3, 9-12, 17-19, 38, 43, 46, 49, 52 and 55-64. Applicant's arguments and the Declaration of Dr. Abad, both filed 21 January 2005, have been fully considered but they are not persuasive.

Applicant urges that limiting the claims to only the exact exemplary sequences is unreasonable because it is relatively simple to modify a nucleic acid and amino acid sequence at a few positions to generate a protein that retains the full activity of the original, and would not give Applicant any meaningful protection (response pg 7-8).

This is not found persuasive. The claims <sup>are</sup> not drawn to modification of only a few positions, but to modification of up to 362 nucleotides or amino acids. If, as Applicant contends, it is “relatively simple” to modify 362 nucleotides, then it would also be “relatively simple” to modify 363 nucleotides, thus avoiding the scope of the claim. Thus, applicant’s argument about teaching the public to make and use the invention without obtaining any protection it contradictory to Applicant’s argument that nucleic acids with 90% identity to SEQ ID NO:1 are enabled.

Applicant urges that claims to nucleic acids with 93%, 94% and 95% identity would meet the patentability requirements even if specified percentages well below 90%; these claims have been ignored, however (response pg 8).

This is not found persuasive. Nucleic acids that have 93% identity to SEQ ID NO:1 would have up to 253 nucleotide substitutions and up to 253 amino acid substitutions, nucleic acids that have 94% identity to SEQ ID NO:1 would have up to 217 nucleotide substitutions and up to 217 amino acid substitutions, and nucleic acids that have 95% identity to SEQ ID NO:1 would have up to 181 nucleotide substitutions and up to 181 amino acid substitutions. The specification does not teach how to make nucleic acids encoding pesticidal proteins with 181, 217 or 253 substitutions.

Applicant urges that guidance is provided as to what sequence alterations may be made and still provide a pesticidal polypeptide; endotoxin genes are well known in the art, an

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exemplary sequence was provided, the claimed sequences differ from the exemplary by structural parameters, and guidance for determining percent identity is given on pg 33-38 (response pg 9).

This is not found persuasive because the specification does not teach how to make nucleic acids encoding Coleopteran pesticidal proteins with 181, 217, 253 or 362 substitutions. Guidance for determining percent identity does not teach the necessary and sufficient structural features of the claimed nucleic acids

Applicant urges that support is provided for the functional limitation, guidance is provided in that the alterations should be conservation substitutions and have particular activity. Applicant urges that while not every nucleic acid that meets the identity limitations will have the function, one of skill in the art could make and use the nucleic acids because methods for assaying pesticidal activity are routine and demonstrated in the specification (response pg 10).

This is not found persuasive because the specification only suggests inserting trypsin and chymotrypsin digestion sites and suggests making variants by deleting, substituting or inserting one or more amino acids, but do not provide guidance as to which amino acids to delete, substitute or insert, other than the insertion of a few amino acids. The specification does not teach how to make nucleic acids encoding Coleopteran pesticidal proteins with 181, 217, 253 or 362 substitutions. Variants within the full scope of the claims are not taught.

Applicant urges that Bt toxins are very well-characterized, and that the specification uses Li et al for guidance in making mutations in the Cry8-like proteins, as in Example 6; thus, adequate guidance is provided (response pg 10-11).

This is not found persuasive. Li et al only provided guidance for making truncations and insertion of chymotrypsin cleavage sites; Li et al do not provide guidance for making 181, 217,

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253 or 362 amino acid substitutions in a 1206 amino acid protein. Furthermore, the protein taught by Li et al is a cry3Aa protein, not a Cry8 protein.

Applicant urges that Li et al teaches the tertiary structure of an exemplary Cry endotoxin, and the instant inventors were able to use the extensive knowledge in the art to modify the exemplary sequences to make variant endotoxins (response pg 11-12).

This is not found persuasive because the instant inventors did not use Li et al to make 181, 217, 253 or 362 amino acid substitutions in a 1206 amino acid protein to create a Coleopteran pesticidal protein.

Applicant urges that those of skill in the art are aware of conserved regions of the Cry endotoxins and can use the Pfam database to determine protein function and conserved regions and regions that are more likely to tolerate mutations (response pg 12).

This is not found persuasive. This database search provides no guidance as to the relevance to the sequence segments that are responsible for the pesticidal specificity of the proteins (see Li et al, pg 815, left column). Additionally, the Pfam database results sent by Applicant give no indication what, if any, of the information sent was available in the database at the time of filing. Lastly, the specification does not teach using this database. See *Genentech, Inc. v. Novo Nordisk, A/S*, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997), which teaches that disclosure of a “mere germ of an idea does not constitute [an] enabling disclosure”, and that “the specification, not the knowledge of one skilled in the art” must supply the enabling aspects of the invention.

Applicant urges that the specification teaches several nucleic acids with low percent identity to SEQ ID NO:1 but that encode pesticidal proteins. In Examples 4 and 6, truncated proteins encoded by SEQ ID NO:15 and 19 are described; they have 55% and 51% identity to

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SEQ ID NO:1, respectively, and is structurally very different from SEQ ID NO:1 (response pg 12-13).

This is not found persuasive. The specification teaches a fragment, in the form of SEQ ID NO:15, but does not teach an additional sequence. While the query match similarity between the truncated proteins encoded by SEQ ID NO:15 and 19 may be 55% and 51% to SEQ ID NO:1, respectively, the query match value is affected by differences in length of the sequences. One of skill in the art would not consider a truncated protein as having 55% identity over its entire length, but would only look at it as a truncated protein. The local match similarity between SEQ ID NO:15 and the first half of SEQ ID NO:1 is 100%; thus SEQ ID NO:15 does not teach which 181, 217, 253 or 362 amino acids to substitute in SEQ ID NO:2.

Applicant urges that Example 6 also teaches the truncated protein encoded by SEQ ID NO:11 which also has a four amino insertion in it; SEQ ID NO:11 has 56% identity to SEQ ID NO:1. Applicant also urges that the specification teaches a maize-optimized sequence that encodes SEQ ID NO:16 but has less than 69% identity to SEQ ID NO:15 (response pg 13-14).

This is not found persuasive. SEQ ID NO:11 only provides guidance for a single insertion of 4 amino acids in the 669 amino acid long SEQ ID NO:16 and does not provide guidance for nucleic acids encoding proteins with 70% identity to SEQ ID NO:2, which nucleic acids with 90% identity to SEQ ID NO:1 encompass). No amino acid substitutions were made in the protein sequence encoded by SEQ ID NO:15. Nucleic acids encoding SEQ ID NO:16 are enabled, and this is true regardless of their identity to SEQ ID NO:15. What is not enabled is nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions relative to SEQ ID NO:2.

Applicant urges that the specification does not teach only a fragment and a single 4 amino acid substitution and has not provided guidance for making up to 362 amino acid substitutions, as they have provided percent identity variants that include both fragments and amino acid changes and have taught representative species of the genus; furthermore there is extensive knowledge in the art about the structure and function of endotoxins, thus equipping one of skill in the art to identify which portions of the disclosed sequence are more conserved and which would tolerate mutations (response pg 14).

This is not found persuasive because the percent identity variants taught by the specification do not represent the full scope of the claims. Making a fragment and a single 4 amino acid substitution are not the same thing as making 362 amino acid substitutions. It is “the specification, not the knowledge of one skilled in the art” that must supply the enabling aspects of the invention (*Genentech, Inc. v. Novo Nordisk, A/S*, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997)).

Applicant urges that the amount of experimentation required is not undue as provided by the working examples and reports in the art of similar experimentation, citing Wu et al (response pg ).

This is not found persuasive. Wu et al only modified 4 amino acids, not 181, 217, 253 or 362 amino acids. None of the working examples in the specification modified 181, 217, 253 or 362 amino acids.

Applicant urges that the quality of experimentation required to make the claimed nucleic acids amounts to two steps, making the nucleic acid and assaying the encoded protein for activity; thus, experimentation is not undue, and provide the Declaration of Dr. Abad (response pg 15).

This is not found persuasive. Assays for the protein are more detailed than assays for enzymatic activity; the latter can often be easily assayed spectrophotographically. The assays



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detailed in Examples 4, 6 and 7 require expressing the proteins in *E. coli*, purifying the protein from large scale cultures of the bacteria via affinity chromatography followed by extensive dialysis, and incorporating the protein into the diets of rootworms in replicates of 4, with mortality measured on the 4<sup>th</sup> to 7<sup>th</sup> day (Examples 4, 6 and 7); thus, each assay requires up to two weeks and large quantities of materials. As guidance is not provided for making up to 362 amino acid substitutions in a 1206 amino acid protein, undue trial and error experimentation would be required to make and to assay vast numbers of nucleic acids in order to find any that fell within the scope of the claims.

Dr. Abad states that he would be able to make and use the claimed nucleic acids by making nucleic acids with 90% identity to SEQ ID NO:1 and assaying the activity of the encoded protein and would consider this experimentation routine. It is also his understanding that proteins can be produced that share a relatively low degree of sequence identity, maybe even as low as 70% identity (Declaration ¶2-3).

This is not found persuasive. The Declaration only provides opinions, and ones the Declarant is not even sure of.

Applicant urges that the amount of experimentation required to practice the identity claims is not undue, because plant transformation and DNA constructs are routine (response pg 15-16).

This is not found persuasive. Plant transformation and construct of DNA constructs, per se, are enabled. What is not enabled is making the nucleic acids required to make the claimed plants and constructs, that is nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions in a 1206 amino acid protein, given the lack of guidance provided in the specification.

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Applicant urges that it is customary in the art to make and assay sequences, for example by shuffling, as described in US 5,837,458. Applicant also cites Minshull et al and Christians et al, and urges that these methods are designed to generate and test a very large number of variant sequences (response pg 16).

This is not found persuasive. With respect to using DNA shuffling, the specification, on pg 29, suggests using GenBank U04365, which is identical to SEQ ID NO:3 of Michaels et al (1996, US Patent 5,554,534), as the other nucleic acid in shuffling; however, this sequence encodes a protein with 79.8% identity to the instant SEQ ID NO:2. Thus, it is unlikely that it could be used to generate a nucleic acid that encodes a protein with 70% identity to SEQ ID NO:2. Christians et al did not produce proteins with only 70% identity to the starting protein (see paragraph spanning pg 260-261). Minshull et al teaches that a population should be used as the starting material (pg 284, right column, paragraph 4); the specification does not teach such a population. Minshull et al also teaches that the activities of chimeric enzymes are not predictable simply by comparing those of the parent enzymes (paragraph spanning pg 288-289); thus, , even if the population of starting materials has been provided, making nucleic acids that encode proteins pesticidal to coleopterans and have substitutions within the full scope of the claims is not predictable. could not be considered because they were not sent.

Applicant urges that inoperative embodiments do not render the claims invalid and undue experimentation would not required to test a protein for pesticidal activity; Lazar et al and Hill et al illustrate that one would be able to determine whether a particular sequence change affected the function of a protein (response pg 17-18).

This is not found persuasive. As discussed above, undue trial and error experimentation would be required to make and to assay vast numbers of nucleic acids in order to find any that

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fell within the scope of the claims. Neither Lazar et al nor Hill et al needed to engage in undue trial and error experimentation; thus, their use in response to an argument about trial and error experimentation is off point.

Applicant urges that in Wands the experimentation required was not found undue (response pg 18-19).

This is not found persuasive because making all possible single amino acid substitutions, in an 3621 nucleotide long nucleic acid like that of SEQ ID NO:1 would require making and analyzing  $19^{3621}$  nucleic acids; these nucleic acids would have about 99.99% identity to SEQ ID NO:1. Making the nucleic acids this way would be required because of the lack of guidance provided in the specification. Thus, in the instant case, the amount of experimentation required would be undue.

It is noted that the specification teaches does not teach nucleic acids comprising 50 nucleotide segments of SEQ ID NO:1 within the full scope of the claims. The only such molecules taught in the specification are SEQ ID NO:15 and 19.

5. Claims 1-3, 9-12, 17-19, 38, 43, 46, 49, 52 and 55-65 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The rejection is repeated for the reasons of record as set forth in the Office action mailed 21 October 2004, as applied to claims 1-3, 9-12, 17-19, 38, 42-43, 46, 48-49, 52 and 54-64. Applicant's arguments filed 21 January 2005 have been fully considered but they are not persuasive.

Applicant urges that that because the claimed nucleic acids are defined in relation to SEQ ID NO:1, they have provided a structural definition of the sequences, and because they have

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provide assays for one of skill in that to assess whether those sequences meet the functional limitation of the claims, they have met the requirements of *Eli Lilly* and *Amgen*, also citing *Amgen vs Hoechst, Moba* and *Enzo* (response pg 20-21).

This is not found persuasive. *Eli Lilly* at pg 1406 states "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." A single nucleic acid of SEQ ID NO:1 does not constitute a significant portion of the genus of nucleic acids with 90% identity to SEQ ID NO:1. The specification does not describe the structural features that distinguish nucleic acids with 90% identity to SEQ ID NO:1 that encode pesticidal proteins from nucleic acids with 90% identity to SEQ ID NO:1 that do not encode pesticidal proteins. *Enzo* states that a deposited sequence meets the written description requirement; no nucleic acid with 90% identity to a known sequence and that encodes a protein with 70% identity to the original protein has been deposited by Applicant, nor has any other nucleic acid within the scope of the claims. In the instant case the knowledge of the art the disclosed function is not sufficiently correlated to a particular, known structure; which 362 amino acids can be substituted in SEQ ID NO:2 is unknown.

Applicant urges that Bt toxins are very well-characterized, and that the specification uses Li et al for guidance in making mutations in the Cry8-like proteins, as in Example 6; thus, adequate guidance is provided (response pg 21-22).

This is not found persuasive. Li et al only provided guidance for making truncations and insertion of chymotrypsin cleavage sites; Li et al do not provide guidance for making 362 amino

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acid substitutions in a 1206 amino acid protein. Additionally, Applicant's arguments are drawn to an enablement rejection, not a written description rejection.

Applicant urges that one of skill in the art could use the Pfam database to make the claimed nucleic acids, thus they have envisioned the detailed construction of the gene (response pg 22).

This is not found persuasive. The specification does not describe the necessary and sufficient structural features for nucleic acids with 90% identity to SEQ ID NO:1 and that encode a protein that is pesticidal to Coleopterans within the full scope of the claims, and from what was sent in Appendix B, neither does the Pfam database. Additionally, the Pfam database results sent by Applicant give no indication what, if any, of the information sent was available in the database at the time of filing.

Applicant urges that the specification describes several nucleic acids with low percent identity to SEQ ID NO:1 but that encode pesticidal proteins. In Examples 4 and 6, truncated proteins encoded by SEQ ID NO:15 and 19 are described; they have 55% and 51% identity to SEQ ID NO:1, respectively. Example 6 also teaches the truncated protein encoded by SEQ ID NO:11 which also has a four amino insertion in it; SEQ ID NO:11 has 56% identity to SEQ ID NO:1. Applicant also urges that the specification teaches a maize-optimized sequence that encodes SEQ ID NO:16 but has less than 69% identity to SEQ ID NO:15 (response pg 23).

This is not found persuasive. The Office is not dismissing the teachings in the specification with regard to the fragments and variant taught in the specification; the Office is saying that they are not sufficient to describe nucleic acid within the full scope of the claims. While the query match similarity may be 55%, the query match value is affected by differences in length of the sequences. No amino acid substitutions were made in the protein sequence

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encoded by SEQ ID NO:15, thus, this nucleic acid does not describe nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions relative to SEQ ID NO:2.

Applicant urges that they disagree with the assessment of the significance exemplary proteins, so that one of skill in the art would recognize what portions of the protein are most significant (response pg 23-24).

This is not found persuasive. The claims encompass nucleic acids encoding proteins with 181, 217, 253 or 362 amino acid substitutions relative to SEQ ID NO:2. The specification does not describe such nucleic acid within the full scope of the claims. Where does the specification describe such a nucleic acid?

### ***Claim Rejections - 35 USC § 102***

6. Claim 65 is rejected under 35 U.S.C. 102(b) as being anticipated by Michaels et al (US Patent 5,556,534).

Michaels et al teach a nucleic acid that comprises 50 nucleotides of SEQ ID NO:1 and encodes a protein that is pesticidal for Coleopterans (see search results).

7. Claims 39-40, 44-45 and 50-51 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

### ***Conclusion***

8. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

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A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (571) 272-0801. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached at (571) 272-0804. The central fax number for official correspondence is (571) 273-8300.

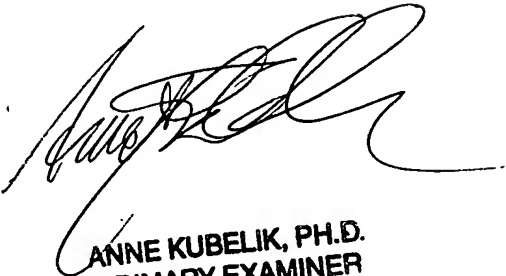
Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

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Anne R. Kubelik, Ph.D.

April 15, 2005



ANNE KUBELIK, PH.D.  
PRIMARY EXAMINER

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OM nucleotide - nucleotide search, using sw model

Run on: January 7, 2003, 00:49:27 (Search time 89 seconds  
(without alignments)  
12477.265 Million cell updates/sec)

File: US-10-032-717-1

Perfect score: 3621  
Sequence: 1 atgagcccaatacaatacaaa.....cgatcgagcgagcgagtaaa 3621

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 682724

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2565.2	70.8	3507	1	US-08-315-468-3
2	1812.2	50.0	3471	1	US-07-876-280-29
3	1812.2	50.0	3471	1	US-07-812-180A-1
4	1812.2	50.0	3471	1	US-08-315-468-1
5	1812.2	50.0	3471	4	US-07-941-650A-1
6	1180	32.6	3797	1	US-07-915-203-1
7	1180	32.6	3797	1	US-08-272-887-1
8	1180	32.6	3797	1	US-08-789-449-1
9	883.4	24.4	4344	2	US-08-532-547-4
10	883.4	24.4	4344	2	US-08-379-656B-4
11	883.4	24.4	4344	3	US-08-455-838-4
12	883.4	24.4	4344	3	US-09-013-809-4
13	883.4	24.4	4344	4	US-09-471-177-4
14	882.8	24.4	3471	4	US-09-002-285-73
15	848.6	23.4	3759	1	US-08-543-921-1
16	848.6	23.4	3759	2	US-08-880-685-1
17	848.6	23.4	3759	2	US-08-880-684-1
18	822.2	22.7	3453	4	US-09-002-285-75
19	734.2	20.3	3411	4	US-09-002-285-77
20	733.6	20.3	3411	1	US-07-973-330-3
21	731.4	20.2	3334	1	US-08-100-709-3
22	678	18.7	3934	1	US-08-176-865-3
23	678	18.7	3934	1	US-08-474-038-3
24	678	18.7	3934	2	US-08-776-046-3
25	678	18.7	3934	2	US-08-881-340-3
26	678	18.7	3934	2	US-08-881-340-3
27	673.6	18.6	4074	1	US-08-377-650-1

28	659.2	18.2	3684	1	US-08-448-170-7
29	659.2	18.2	3684	3	US-08-861-603-5
30	618.6	17.1	3567	6	US188960-5
31	615.4	17.0	3567	2	US-08-980-071-5
32	615.4	17.0	3567	2	US-08-980-071-5
33	615.4	17.0	3567	2	US-08-980-071-5
34	615.4	17.0	3567	2	US-08-980-071-5
35	615.4	17.0	3567	3	US-09-314-093-5
36	615.4	17.0	3567	3	US-09-314-093-5
37	615.4	17.0	3567	3	US-09-250-848-5
38	615.4	17.0	3567	4	US-09-251-885-5
39	615.4	17.0	3567	4	US-09-337-635-5
40	615.4	17.0	3567	4	US-09-337-635-5
41	615.4	17.0	3567	4	US-09-337-635-5
42	613.8	17.0	3567	4	US-09-337-280-5
43	613.8	17.0	3567	2	US-08-980-071-9
44	613.8	17.0	3567	2	US-08-980-071-9
45	613.8	17.0	3567	2	US-08-980-071-11

## ALIGNMENTS

RESULT 1  
US-08-315-468-3  
Sequence 3, Application US/08315468  
Patent No. 5554534  
GENERAL INFORMATION:  
APPLICANT: Michaels, Tracy Ellis  
APPLICANT: Foncecrade, Luis  
TITLE OF INVENTION: Process for Controlling Search Pease  
TITLE OF INVENTION: With Bacillus thuringiensis Isolates  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentia Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/315,468  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,941  
FILING DATE: 01 FEB 1993  
APPLICATION NUMBER: 07/828,430  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/808,316  
FILING DATE: 16-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M473.C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
FAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3507 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO





Db	3046	CGAAGCGCTATCCAAATGAGATTAACCGAAATTAAGTAAATGGATATACACATTT	2105
Oy	3121	GGCTGAGTAAGTACAAACAATCATATCATCTGCTCTTGATATCCAACTGGCATATGG	3180
Db	3106	GGGTGATATGTACACAAATCAATCAATCATCTGCTCTTGATATCCAACTGAAATGAA	3165
Oy	3181	CAGTTTCCCAACAGTTTACGTTCAACCGAATCAAGATATGTGTATCGAGTTACTGCG	3240
Db	3166	CAATTTCCAAAGTTTACAGTTCAACCGAATCAAGATATGTGTATCGAGTTACTGCA	3225
Oy	3241	AGAAAAGAAAGGCTATGCAATATGATATCTCTGATGCTGAAATCCAAACAGAA	3300
Db	3226	AGAAAAGAAAGGCTATGCAATATGATATCTCTGATGCTGAAATCCAAATCAGAA	3285
Oy	3301	ACGCTTACTTTAGTCGACACGATATATGATACAAATGGAATGTAATACGACAGTGTCG	3360
Db	3386	ACGCTTACTTTAGTCGACACGATATATGATACAAATGGAATGTAATACGACAGTGTCG	3344
Oy	3361	AATACAAATGATATTAACAATAATATGCTATATTAACAACGATCTCACTACA	3414
Db	3346	AATACAAACGATATTAACAATAATATGCTATATTAACAACGCTTATATCTA	3399

## US-07-876-280-25

Sequence 29, Application US/0786280  
Patent No. 5262158  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel M.  
APPLICANT: Cannon, Raymond J. C.  
APPLICANT: Bagley, Angela L.  
TITLE OF INVENTION: No. 5262158c1 Bacillus thuringiensis isolates for  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Sallawachuk  
STREET: 2421 N.W. 11st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/876,280  
FILING DATE: 19920430  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sallawachuk, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/S 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3471 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
STRAIN: kumamotoensis  
INDIVIDUAL ISOLATES: P550C  
IMMEDIATE SOURCE:  
CLONING: E. coli NM522(pMTC3230) NRRL B-18769